Amendment to the Claims

This listing of claims will replace all prior versions and listings of claims in the above-referenced application.

1. (currently amended) A transgenic *C. elegans* nematode, the cells of which contain a transgene comprising a regulatory element of the *C. elegans vap-1* [[a]] gene ~~that encodes a nematode secretory product or a homolog thereof~~ operably linked to a DNA sequence encoding a detectable marker, wherein the detectable marker is expressed in a *C. elegans* ~~pharyngeal gland cell or~~ amphid sheath cell.

2. (currently amended) The transgenic nematode of claim 1, wherein the transgene further comprises at least a portion of the coding sequence of the *C. elegans vap-1* gene.

3. (currently amended) The transgenic nematode of claim 2, wherein the transgene further comprises at least a portion of an intron from the *C. elegans vap-1* gene.

4. (currently amended) The transgenic nematode of claim 2, wherein the transgene further comprises at least a portion of the 3' untranslated region from the *C. elegans vap-1* gene.

5. (original) The transgenic nematode of claim 2, wherein the coding sequence of the *C. elegans vap-1* gene is in frame with the sequence encoding the detectable marker.

6. (original) The transgenic nematode of claim 1, wherein the transgene is contained in a chromosome.

7. (original) The transgenic nematode of claim 1, wherein the transgene is extrachromosomal.

8. (original) The transgenic nematode of claim 5, wherein the transgene comprises an integrated array comprising a second regulatory element operably linked to a second copy of a DNA sequence encoding the detectable marker.

9. (original) The transgenic nematode of claim 8, wherein the second regulatory element directs expression of the detectable marker in a substantially different population of cells to that in which the first regulatory element directs expression of the detectable marker.

10. (original) The transgenic nematode of claim 1, wherein the nematode secretory product is a protein.

11. (original) The transgenic nematode of claim 1, wherein the detectable marker is selected from the list consisting of: a fluorescent polypeptide, a chemiluminescent polypeptide, an epitope tag, and an enzyme.

12. (previously presented) The transgenic nematode of claim 1, wherein the detectable marker is selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag.

13. (previously presented) The transgenic nematode of claim 1, wherein the detectable marker comprises a variant of a marker selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag, wherein the variant is detectable using the same detection means by which the marker of which it is a variant is detectable.

14-24. (canceled)

25. (previously presented) The transgenic nematode of claim 1, wherein the regulatory element is a 5' regulatory region comprising between 1 nucleotide and 10 kB of sequence extending in a 5' direction from the start codon of the *C. elegans vap-1* gene.

26-45. (canceled)

46. (currently amended) A method of generating a nematode comprising steps of:

(a) selecting a parasitic nematode secretory protein;

(b) identifying a *C. elegans* homolog of the protein selected in step (a), wherein the *C. elegans* homolog is a *C. elegans* secretory product;

(c) identifying a nucleic acid sequence comprising a regulatory region of a *C. elegans* gene encoding the *C. elegans* homolog identified in step (b); and

(d) generating a transgenic *C. elegans* nematode, wherein cells of the transgenic nematode comprise a nucleic acid sequence including the identified regulatory region operably linked to a nucleic acid sequence encoding a detectable marker, wherein the detectable marker is expressed in a pharyngeal gland cell or amphid sheath cell.

47. (currently amended) The method of claim 46, wherein the parasitic nematode is a member of an order selected from the group consisting of the *Strongylida*, *Rhabditida*, *Ascaridida*, *Spirurida*, *Oxyurida*, *Enoplida*, *Tylenchida*, or *Dorylaimida* nematode orders ~~a *Tylenchid* nematode~~.

48. (original) The method of claim 46, wherein the regulatory region comprises a promoter of the *C. elegans* homolog identified in step (b).

49. (original) The method of claim 46, wherein the nucleic acid sequence of step (d) includes at least a portion of the coding sequence of a gene encoding the *C. elegans* homolog of part (c).

50. (original) The method of claim 49, wherein the nucleic acid sequence of step (d) includes a signal sequence.

51. (original) The method of claim 49, wherein the nucleic acid sequence of step (d) includes at least a portion of an intron from a gene encoding the *C. elegans* homolog of part (c).

52. (original) The method of claim 49, wherein the nucleic acid sequence of step (d) includes at least a portion of the 3' untranslated region from a gene encoding the *C. elegans* homolog of part (c).

53. (original) The method of claim 46, wherein the regulatory region is sufficient to direct expression of the nucleic acid of step (d).

54-105. (canceled)

106. (currently amended) A method of expressing a ~~first~~ polynucleotide in a *C. elegans* nematode comprising the step of:

generating a transgenic *C. elegans* nematode, cells of which comprise a transgene comprising a *vap-1* regulatory region operably linked to the ~~first~~ polynucleotide; and

maintaining the *C. elegans* nematode so that expression of the ~~first~~ polynucleotide occurs in an amphid sheath cell.

107. (previously presented) The method of claim 106, wherein the polynucleotide encodes a polypeptide.

108. (previously presented) The method of claim 106, wherein the transgene comprises between 1 nucleotide and 10kB of sequence extending in a 5' direction from the start codon of the *C. elegans vap-1* gene.

109. (previously presented) The method of claim 106, wherein the generating step comprises injecting a polynucleotide into a *C. elegans* nematode, wherein the polynucleotide comprises a *vap-1* regulatory region operably linked to the polynucleotide.

110-114. (canceled)

115. (currently amended) A method of generating a transgenic *C. elegans* nematode comprising steps of:

(a) selecting a parasitic nematode secretory protein that is expressed in a pharyngeal gland cell [[,]] or an amphidial gland cell~~, or both,~~ of a parasitic nematode;

(b) identifying a *C. elegans* homolog of the protein selected in step (a); and

(c) generating a transgenic *C. elegans* nematode, wherein cells of the transgenic nematode comprise a ~~first~~ DNA element encoding a detectable marker operably linked to a

regulatory sequence ~~second DNA element whose sequence comprises a sequence located up to 10 kb immediately upstream of the start codon~~ of the gene that encodes the *C. elegans* homolog.

116. (currently amended) The method of claim 115, wherein the regulatory sequence is ~~A transgenic *C. elegans* nematode, cells of which comprise a first DNA element encoding a detectable marker operably linked to a second DNA element whose sequence comprises a sequence~~ located ~~up to 10 kb immediately~~ upstream of the start codon of the [[a]] gene that encodes a *C. elegans* homolog of a parasitic nematode secretory protein~~, which parasitic nematode secretory protein is expressed in a pharyngeal gland cell, an amphidial gland cell, or both, of a parasitic nematode~~.

117. (currently amended) The method ~~transgenic nematode~~ of claim 115 ~~116~~, wherein the ~~sequence~~ transgene includes ~~of the second DNA element comprises a sequence located~~ up to 8 kB of genomic sequence immediately upstream of the start codon of the gene that encodes the *C. elegans* homolog.

118. (currently amended) The method ~~transgenic nematode~~ of claim 115 ~~116~~, wherein the ~~sequence~~ transgene includes ~~of the second DNA element comprises a sequence located~~ up to 6 kB of genomic sequence immediately upstream of the start codon of the gene that encodes the *C. elegans* homolog.

119-121. (canceled)

122. (currently amended) The method ~~transgenic nematode~~ of claim 115 ~~116~~, wherein the transgene is integrated into the genome of the transgenic *C. elegans* nematode.

123. (currently amended) The method ~~transgenic nematode~~ of claim 115 ~~116~~, wherein the transgene ~~further~~ comprises at least a portion of the coding sequence of the gene that encodes the *C. elegans* secretory protein, at least a portion of an intron of the gene that encodes the *C. elegans* secretory protein, at least a portion of a 3' untranslated region of the gene that encodes the *C. elegans* secretory protein, or a combination of any of the foregoing.

124. (currently amended) A method of generating a transgenic *C. elegans* nematode comprising steps of:

(a) selecting a *C. elegans* secretory protein that is expressed in a pharyngeal gland cell [[,]] or an amphid sheath cell~~, or both~~; and

(b) generating a transgenic *C. elegans* nematode, wherein cells of the transgenic nematode comprise a transgene comprising a ~~first~~ DNA element that encodes a detectable marker operably linked to a regulatory ~~second DNA element whose sequence comprises a~~ sequence ~~located up to 10 kb immediately upstream of the start codon~~ of the gene that encodes the *C. elegans* secretory protein.

125. (currently amended) The method of claim 124, wherein the regulatory sequence is ~~A transgenic nematode, cells of which comprise a transgene comprising a first DNA element encoding a detectable marker operably linked to a second DNA element whose sequence comprises a sequence~~ located ~~up to 10 kb immediately~~ upstream of the start codon of the [[a]] gene that encodes a *C. elegans* secretory protein.

126. (currently amended) The method of claim 124, wherein the transgene includes ~~The transgenic nematode of claim 125, wherein the sequence of the second DNA element comprises a sequence located~~ up to 8 kB immediately upstream of the start codon of the gene that encodes the *C. elegans* secretory protein.

127. (currently amended) The method of claim 124, wherein the transgene includes ~~The transgenic nematode of claim 125, wherein the sequence of the second DNA element comprises a sequence located~~ up to 6 kB immediately upstream of the start codon of the gene that encodes the *C. elegans* secretory protein.

128. (currently amended) The method of claim 124 ~~The transgenic nematode of claim 125~~, wherein the transgene further comprises at least a portion of the coding sequence of the gene that encodes the *C. elegans* secretory protein, at least a portion of an intron of the gene that encodes a *C. elegans* secretory protein, at least a portion of the 3' untranslated region of the gene that encodes the *C. elegans* secretory protein, or any combination of the foregoing.

129-130. (canceled)

131. (previously presented) The method of claim 106, wherein the polynucleotide encodes a detectable marker.

132. (previously presented) The method of claim 131, wherein the detectable marker is selected from the list consisting of: a fluorescent polypeptide, a chemiluminescent polypeptide, an epitope tag, and an enzyme.

133. (previously presented) The method of claim 131, wherein the detectable marker is selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag.

134. (previously presented) The method of claim 131, wherein the detectable marker comprises a variant of a marker selected from the list consisting of: green fluorescent protein, luciferase, chloramphenicol acetyl transferase, xanthine-guanine phosphoribosyl transferase, beta-galactosidase, horseradish peroxidase, alkaline phosphatase, horseradish peroxidase, alkaline phosphatase, a Myc tag, and an HA tag, wherein the variant is detectable using the same detection means by which the marker of which it is a variant is detectable.

135. (previously presented) The method of claim 131, wherein the detectable marker is alkaline phosphatase.

136. (previously presented) The method of claim 106, wherein the transgene further comprises at least a portion of the coding sequence of the *vap-1* gene, at least a portion of an intron of the *vap-1* gene, at least a portion of the 3' untranslated region of the *vap-1* gene, or any combination of the foregoing.

137 – 142. (canceled)

143. (new) The method of claim 46, wherein the parasitic nematode is a member of a genus selected from the list consisting of the *Haemonchus, Oestertagia, Trichostrongylus, Cooperia, Dictyocaulus, Strongylus, Oesophagostomum, Syngamus, Nematodirus, Heligmosomoides, Nippostrongylus, Metastrongylus, Angiostrongylus, Ancylostoma, Necator, Uncinaria, Bunostomum, Strongyloides, Steinernema, Ascaris, Parascaris, Toxocara, Toxascaris, Baylisascaris, Anisakis, Pseudoterranova, Heterakis, Wuchereria, Brugia, Onchocerca, Dirofilaria, Loa, Thelazia, Dracunculus, Gnathostoma, Enterobius, Oxyuris, Syphacia, Trichinella, Trichuris, Capillaria, Globodera, Heterodera, Meloidogyne, Anguina, Ditylenchus, Hirschmanniella, Naccobus, Pratylenchus, Radopholus, Criconema, Tylenchulus, Paratylenchus, Aphelenchus, Bursaphelenchus, Longidorus, Xiphinema, Trichodorus,* and *Paratrichodorus* nematode genera.